



PATENT APPLICATION

0300

Box/seq.
#15**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Applicant(s): Yoshinaga et al.

Serial No.: 09/728,420

Filed: November 28, 2000

For: Novel Polypeptides Involved in Immune Response

Docket No.: A-579C

RESPONSE TO NOTICE TO COMPLY**AND****ATTORNEY'S STATEMENT PURSUANT TO 37 CFR § 1.821**Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

This is in response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures dated June 7, 2001.

I hereby state that the substitute paper copy and computer readable form (CRF) of the "Sequence Listing" submitted herewith for the above-mentioned patent application are the same, and contain no new matter.

Respectfully submitted,

Robert B. Winter
Attorney/Agent for Applicant(s)
Registration No.: 34,458
Phone: (805) 447-2425
Date: *JUNE 29, 2001*

Please send all future correspondence to:

U.S. Patent Operations/RBW
Dept. 4300, M/S 27-4-A
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One Amgen Center Drive
Thousand Oaks, California 91320-1799

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231, on the date appearing below.

June 28, 2001
DateD. D. O'Fallon
Signature

09728420-070201



SEQUENCE LISTING

<110> Yoshinaga, Steven

Mak, Tak

Shahinian, Arda

Trafuri Bladt, Anna

Senaldi, Giorgio

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<140> 09/728,420

<141> 2000-11-28

<150> PCT/US00/01871

<151> 2000-01-27

<150> US 09/264,527

<151> 1999-03-08

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<151> 1999-02-03

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Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
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 Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp
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Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser		
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Trp Gln Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr
35 40 45
Lys Ser Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His
50 55 60
Leu Ser Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys
65 70 75 80
Asn Val Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met
85 90 95
Asn Thr Ala Thr Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu
100 105 110
Arg Val Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser
115 120 125
Ser Asn Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly
130 135 140
Tyr Pro Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu
145 150 155 160
Ile Asp Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly
165 170 175
Leu Tyr Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly
180 185 190
Asp Val Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr
195 200 205
Ser Ile Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro
210 215 220
Gln Glu Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala
225 230 235 240
Val Leu Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr
245 250 255
Arg Pro His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu
260 265 270
Thr Asp His Ala
275
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<223> Synthetic

<400> 15

Glu Glu Val Ala Met Val Gly Ser Val Leu Ser Cys Pro Phe Leu Tyr
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 Val Tyr Trp Gln Val Thr Tyr Pro Ser Asn Val Asp Ser Tyr Asn Arg
 20 25 30
 Ser Met Gly Phe Ser Leu Leu Asn Val Thr Pro Gln Asp Gln Phe Cys
 35 40 45
 Val Leu Val Leu Val Ala Ala Asn Phe Ser Pro Val Ser Ser Glu Thr
 50 55 60
 Thr Cys Ser Asn Gly Tyr Pro Pro Asn Tyr Trp Ile Asn Thr Asp Asn
 65 70 75 80
 Ser Leu Asp Ala Leu Gln Asn Thr Val Leu Asn Gly Leu Tyr Asp Val
 85 90 95
 Ser Leu Arg Thr Cys Cys Glu Asn Val Leu Gln Asn Thr Ser Gln Gly
 100 105 110
 Lys Lys Leu Ala Val Leu Val Ile Arg Arg Ser Tyr Gly
 115 120 125

<210> 16

<211> 1294

<212> DNA

<213> Homo sapiens

<220>

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<220>

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<222> (200)..(1105)

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tctccgcggg	cccaagttct	ccgcgccccg	aggtctccgc	gccccgaggt	ctccgcggcc	180	
cgaggtctcc	gccccacc	atg cgg ctg ggc agt cct gga ctg ctc ttc ctg	Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu	1	5	10	232
ctc ttc agc agc	ctt cga gct gat	act cag gag aag gaa gtc aga gcg	Leu Phe Ser Ser Leu Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala	15	20	25	280
atg gta ggc agc	gac gtg gag ctc	agc tgc gct tgc cct gaa gga agc	Met Val Gly Ser Asp Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser	30	35	40	328
cgt ttt gat tta	aat gat gtt tac	gta tat tgg caa acc agt gag tcg	Arg Phe Asp Leu Asn Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser	45	50	55	376
aaa acc gtg gtg	acc tac cac atc	cca cag aac agc tcc ttg gaa aac	Lys Thr Val Val Thr Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn	60	65	70	424
gtg gac agc cgc	tac cgg aac cga gcc	ctg atg tca ccg gcc ggc atg	Val Asp Ser Arg Tyr Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met	80	85	90	472
ctg cgg ggc gac	ttc tcc ctg cgc	ttg ttc aac gtc acc ccc cag gac	Leu Arg Gly Asp Phe Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp	95	100	105	520
gag cag aag ttt	cac tgc ctg gtg	ttg agc caa tcc ctg gga ttc cag	Glu Gln Lys Phe His Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln	110	115	120	568
gag gtt ttg agc	gtt gag gtt aca	ctg cat gtg gca gca aac ttc agc	Glu Val Leu Ser Val Glu Val Thr Leu His Val Ala Ala Asn Phe Ser	125	130	135	616
gtg ccc gtc gtc	agc gcc ccc cac	agc ccc tcc cag gat gag ctc acc	Val Pro Val Val Ser Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr	140	145	150	664
ttc acg tgt aca	tcc ata aac ggc	tac ccc agg ccc aac gtg tac tgg	Phe Thr Cys Thr Ser Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp	160	165	170	712
atc aat aag acg	gac aac agc ctg	ctg gac cag gct ctg cag aat gac	Ile Asn Lys Thr Asp Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp	175	180	185	760
acc gtc ttc ttg	aac atg cgg ggc	ttg tat gac gtg gtc agc gtg ctg	Thr Val Phe Leu Asn Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu	190	195	200	808
agg atc gca cgg	acc ccc agc gtg	aac att ggc tgc tgc ata gag aac	Arg Ile Ala Arg Thr Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn	205	210	215	856
gtg ctt ctg cag	cag aac ctg act	gtc ggc agc cag aca gga aat gac	Val Leu Leu Gln Gln Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp	220	225	230	904
atc gga gag aga	gac aag atc aca	gag aat cca gtc agt acc ggc gag					952

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Ile Gly Glu Arg Asp Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu	
240 245 250	
aaa aac gcg gcc acg tgg agc atc ctg gct gtc ctg tgc ctg ctt gtg	1000
Lys Asn Ala Ala Thr Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val	
255 260 265	
gtc gtg gcg gtg gcc ata ggc tgg gtg tgc agg gac cga tgc ctc caa	1048
Val Val Ala Val Ala Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln	
270 275 280	
cac agc tat gca ggt gcc tgg gct gtg agt ccg gag aca gag ctc act	1096
His Ser Tyr Ala Gly Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr	
285 290 295	
ggc cac gtt tgaccggagc tcaccgccca gagcgtggac agggcttccg	1145
Gly His Val	
300	
tgagacgccca ccgtgagagg ccaggtggca gcttgagcat ggactcccag actgcagggg	1205
agcacttggg gcagccccca gaaggaccac tgctggatcc cagggagaac ctgctggcgt	1265
tggctgtgat cctggaatga ggccttttc	1294
<210> 17	
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<212> PRT	
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1 5 10 15	
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20 25 30	
Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn	
35 40 45	
Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr	
50 55 60	
Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr	
65 70 75 80	
Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe	
85 90 95	
Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His	
100 105 110	

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Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
145 150 155 160

Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp
165 170 175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
180 185 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
195 200 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
210 215 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225 230 235 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
245 250 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala
260 265 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
275 280 285

Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val
290 295 300

<210> 18

<211> 302

<212> PRT

<213> Homo sapiens

<400> 18

Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu Leu Phe Ser Ser Leu
1 5 10 15

09728420.076001

Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
20 25 30

Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
35 40 45

Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
50 55 60

Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
65 70 75 80

Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
85 90 95

Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His
100 105 110

Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
115 120 125

Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
130 135 140

Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
145 150 155 160

Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp
165 170 175

Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
180 185 190

Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
195 200 205

Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
210 215 220

Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225 230 235 240

Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
245 250 255

Trp Ser Ile Leu Ala Val Leu Cys Leu Leu Val Val Val Ala Val Ala
260 265 270

Ile Gly Trp Val Cys Arg Asp Arg Cys Leu Gln His Ser Tyr Ala Gly
275 280 285

Ala Trp Ala Val Ser Pro Glu Thr Glu Leu Thr Gly His Val
290 295 300

<210> 19

<211> 322

<212> PRT

<213> Mus musculus

00723420-070201

<400> 19

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Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
20 25 30
Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
35 40 45
Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
50 55 60
Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln
65 70 75 80
Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
85 90 95
Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
100 105 110
Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
115 120 125
Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr
130 135 140
Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
145 150 155 160
Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
165 170 175
Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro
180 185 190
Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp
195 200 205
Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr
210 215 220
Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val
225 230 235 240
Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile
245 250 255
Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu
260 265 270
Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu
275 280 285
Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro
290 295 300
His Arg Ser Tyr Thr Gly Pro Lys Thr Val Gln Leu Glu Leu Thr Asp
305 310 315 320

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His Ala

<210> 20

<211> 143

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<223> Synthetic

<400> 20

Met Leu Pro Gly Leu Leu Phe Leu Leu Ser Ser Leu Ala Glu Glu Val
1 5 10 15

Ala Met Val Gly Ser Val Leu Ser Cys Pro Phe Leu Tyr Val Tyr Trp
20 25 30

Gln Val Thr Tyr Pro Ser Asn Val Asp Ser Tyr Asn Arg Ser Met Gly
35 40 45

Phe Ser Leu Leu Asn Val Thr Pro Gln Asp Gln Phe Cys Val Leu Val
50 55 60

Leu Val Ala Ala Asn Phe Ser Pro Val Ser Ser Glu Thr Thr Cys Ser
65 70 75 80

Asn Gly Tyr Pro Pro Asn Tyr Trp Ile Asn Thr Asp Asn Ser Leu Asp
85 90 95

Ala Leu Gln Asn Thr Val Leu Asn Gly Leu Tyr Asp Val Ser Leu Arg
100 105 110

Thr Cys Cys Glu Asn Val Leu Gln Asn Thr Ser Gln Gly Lys Lys Leu
115 120 125

Ala Val Leu Val Ile Arg Arg Ser Tyr Gly Val Glu Leu Thr His
130 135 140

<210> 21

<211> 1370

<212> DNA

<213> Homo sapiens

<220>

<221> 5'UTR

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<222> (1)..(165)

<220>

<221> CDS

<222> (166)..(762)

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tataggaaaa gctgggtacgc ctgcaggtac cgggtccggaa ttcccgggtc gacccacgcg 120
tccgtgaaca ctgaacgcga ggactgttaa ctgtttctgg caaac atg aag tca ggc 177
Met Lys Ser Gly
1
ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa gtt tta aca gga 225
Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys Val Leu Thr Gly
5 10 15 20
gaa atc aat ggt tct gcc aat tat gag atg ttt ata ttt cac aac gga 273
Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly
25 30 35
ggg gta caa att tta tgc aaa tat cct gac att gtc cag caa ttt aaa 321
Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys
40 45 50
atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat ctc act aag aca 369
Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr
55 60 65
aaa gga agt gga aac aca gtg tcc att aag agt ctg aaa ttc tgc cat 417
Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His
70 75 80
tct cag tta tcc aac aac agt gtc tct ttt ttt cta tac aac ttg gac 465
Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp
85 90 95 100
cat tct cat gcc aac tat tac ttc tgc aac cta tca att ttt gat cct 513
His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser Ile Phe Asp Pro
105 110 115
cct cct ttt aaa gta act ctt aca gga gga tat ttg cat att tat gaa 561
Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu His Ile Tyr Glu
120 125 130
tca caa ctt tgt tgc cag ctg aag ttc tgg tta ccc ata gga tgt gca 609
Ser Gln Leu Cys Cys Gln Leu Lys Phe Thr Leu Pro Ile Gly Cys Ala
135 140 145
gcc ttt gtt gta gtc tgc att ttg gga tgc ata ctt att tgt tgg ctt 657
Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu Ile Cys Trp Leu
150 155 160
aca aaa aag aag tat tca tcc agt gtg cac gac cct aac ggt gaa tac 705
Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro Asn Gly Glu Tyr
165 170 175 180

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atg ttc atg aga gca gtg aac aca gcc aaa aaa tct aga ctc aca gat 753
Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser Arg Leu Thr Asp
185 190 195

gtg acc cta taatatggaa ctctggcacc caggeatgaa gcacgttggc 802
Val Thr Leu

cagttttcct caacttgaag tgcaagattc tcttatttcc gggaccacgg agagtctgac 862

ttaactacat acatcttctg ctgggtgttt gtccaatctg gaagaatgac tgtatcagtc 922

aatgggggatt ttaacagact gccttgggtac tgccgagtc tctcaaaaaca aacacctctc 982

tgcaaccagc ttggagagaaa gcccgagctcc tgtgtgctca ctgggagtggt aatccctgtc 1042

tccacatctg ctctagcag tgcatcagcc agtaaaacaa acacatttac aagaaaaatg 1102

ttttaagat gccaggggta ctgaatctgc aaagcaaatg agcagccaag gaccagcadc 1162

tgcccgcatc tcactatcat actacctctt ctttctgtag ggtgagaat tcctctttta 1222

atcagtcagg ggagatgctt caaagctgga gctattttat ttctgagatg ttgatgtgaa 1282

ctgtacatta gtacatactc agtactctcc ttcaattgct gaacccccagt tgaccatttt 1342

accaagactt tagatgcttt cttgtgcc 1370

<210> 22

<211> 199

<212> PRT

<213> Homo sapiens

<400> 22

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
1 5 10 15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
20 25 30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
35 40 45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65 70 75 80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

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Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
115 120 125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
130 135 140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145 150 155 160

Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Val His Asp Pro
165 170 175

Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
180 185 190

Arg Leu Thr Asp Val Thr Leu
195

<210> 23

<211> 199

<212> PRT

<213> Homo sapiens

<400> 23

Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
1 5 10 15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
20 25 30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
35 40 45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
50 55 60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65 70 75 80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
100 105 110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu

00720720.072201

	115						120						125						
His	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Phe	Trp	Leu	Pro				
	130					135					140								
Ile	Gly	Cys	Ala	Ala	Phe	Val	Val	Val	Cys	Ile	Leu	Gly	Cys	Ile	Leu				
	145				150					155					160				
Ile	Cys	Trp	Leu	Thr	Lys	Lys	Lys	Tyr	Ser	Ser	Ser	Val	His	Asp	Pro				
				165					170					175					
Asn	Gly	Glu	Tyr	Met	Phe	Met	Arg	Ala	Val	Asn	Thr	Ala	Lys	Lys	Ser				
			180					185					190						
Arg	Leu	Thr	Asp	Val	Thr	Leu													
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<212>	PRT																		
<213>	Mus musculus																		
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Met	Lys	Pro	Tyr	Phe	Cys	Arg	Val	Phe	Val	Phe	Cys	Phe	Leu	Ile	Arg				
				5					10					15					
Leu	Leu	Thr	Gly	Glu	Ile	Asn	Gly	Ser	Ala	Asp	His	Arg	Met	Phe	Ser				
			20					25					30						
Phe	His	Asn	Gly	Gly	Val	Gln	Ile	Ser	Cys	Lys	Tyr	Pro	Glu	Thr	Val				
		35					40					45							
Gln	Gln	Leu	Lys	Met	Arg	Leu	Phe	Arg	Glu	Arg	Glu	Val	Leu	Cys	Glu				
		50				55					60								
Leu	Thr	Lys	Thr	Lys	Gly	Ser	Gly	Asn	Ala	Val	Ser	Ile	Lys	Asn	Pro				
					70					75					80				
Met	Leu	Cys	Leu	Tyr	His	Leu	Ser	Asn	Asn	Ser	Val	Ser	Phe	Phe	Leu				
				85					90					95					
Asn	Asn	Pro	Asp	Ser	Ser	Gln	Gly	Ser	Tyr	Tyr	Phe	Cys	Ser	Leu	Ser				
			100					105					110						
Ile	Phe	Asp	Pro	Pro	Pro	Phe	Gln	Glu	Arg	Asn	Leu	Ser	Gly	Gly	Tyr				
		115					120					125							
Leu	His	Ile	Tyr	Glu	Ser	Gln	Leu	Cys	Cys	Gln	Leu	Lys	Leu	Trp	Leu				
		130				135					140								
Pro	Val	Gly	Cys	Ala	Ala	Phe	Val	Val	Val	Leu	Leu	Phe	Gly	Cys	Ile				
		145			150					155					160				
Leu	Ile	Ile	Trp	Phe	Ser	Lys	Lys	Lys	Tyr	Gly	Ser	Ser	Val	His	Asp				
				165					170					175					
Pro	Asn	Ser	Glu	Tyr	Met	Phe	Met	Ala	Ala	Val	Asn	Thr	Asn	Lys	Lys				
			180					185					190						

Ser Arg Leu Ala Gly Val Thr Ser
195 200

<210> 25

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<223> Synthetic oglionucleotide

<400> 25
accatgcggc tgggcagtc tgga

24

<210> 26

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<223> Synthetic oglionucleotide

<400> 26
tggtgacctt ccacatccca cag

23

<210> 27

<211> 23

<212> DNA

<213> Artificial sequence

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<223> Synthetic oglionucleotide

<400> 27
tccgatgtca tttcctgtct ggc 23

<210> 28

<211> 24

<212> DNA

<213> Artificial sequence

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<221> misc_feature

<223> Synthetic oglionucleotide

<400> 28
gctctgtctc cggactcaca gccc 24

<210> 29

<211> 28

<212> DNA

<213> Artificial sequence

<220>

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<223> Synthetic oglionucleotide

<400> 29
gtggcagcaa acttcagcgt gcccgctcg 28

<210> 30

<211> 28

<212> DNA

<213> Artificial sequence

<220>

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<223> Synthetic oglionucleotide

<400> 30
cccaacgtgt actggatcaa taagacgg 28

<210> 31

<211> 28

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<223> Synthetic oglionucleotide

<400> 31
gcgtgctgag gatcgacagg accccag 28

<210> 32

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<223> Synthetic oglionucleotide

<400> 32
gcctctagaa agagctggga c 21

<210> 33

<211> 21

<212> DNA

<213> Artificial sequence

<220>

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<221> misc_feature
<223> Synthetic oglionucleotide

<400> 33
cgccgtgttc catttatgag c 21

<210> 34
<211> 18
<212> DNA
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<220>
<221> misc_feature
<223> Synthetic oglionucleotide

<400> 34
gcatatttat gaatccca 18

<210> 35
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